

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Jones, Kenneth A.
Laz, Thomas M.
Borowsky, Beth
- (ii) TITLE OF INVENTION: DNA Encoding a GABABR2 Polypeptide And
Uses Thereof
- (iii) NUMBER OF SEQUENCES: 47
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: Not Yet Known
(B) FILING DATE: Herewith
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: White Esq., John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 54002-D
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 212-278-0400
(B) TELEFAX: 212-391-0525

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 3244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TGACCTCGGG GCAGGTCCTG GTGCAGAGCG TCGCCAAGGA CGCCGAGAGG GAGGCGGGAT	60
TGCCCAGACA TCCTTCAGCG AAGTGCATGT GTGTTTGTA ACCATCGTTG GCTGTCGGGA	120
GACCGCGAGG ACCGGTCCAG GCTGCGGCGG AGTCGAGGGC GAGGGAGAGG CCGCGTGAGT	180

092475-121599

GAGCAGAGTC	CAGAGCCGTG	CGCCCCCAGA	ACTGCGCGTC	CGCCCCGTGC	ACCCCCGCGC	240
GCCATGCCCA	GTTGCCCCGC	GCGCTCTGCT	ACGGGCCCCG	TCTCCATCAT	GGGCCTCATG	300
CCGCTCACCA	AGGAGGTGGC	CAAGGGCAGC	ATCGGGCGCG	GTGTGCTCCC	CGCCGTGGAA	360
CTGGCCATCG	AGCAGATCCG	CAACGAGTCA	CTCCTGCGCC	CCTACTTCCT	CGACCTGCGG	420
CTCTATGACA	CGGAGTGCGA	CAACGCAAAA	GGGTTGAAAG	CCTTCTACGA	TGCGATAAAA	480
TACGGGCCGA	ACCACTTGAT	GGTGTTTGGA	GGCGTCTGTC	CATCCGTCAC	ATCCATCATT	540
GCAGAGTCCC	TCCAAGGCTG	GAATCTGGTG	CAGCTTTCTT	TTGCTGCAAC	CACGCCTGTT	600
CTAGCCGATA	AGAAAAAATA	CCCTTATTTT	TTTCGGACCG	TCCCATCAGA	CAATGCGGTG	660
AATCCAGCCA	TTCTGAAGTT	GCTCAAGCAC	TACCAGTGGA	AGCGCGTGGG	CACGCTGACG	720
CAAGACGTTC	AGAGGTTCTC	TGAGGTGCGG	AATGACCTGA	CTGGAGTTCT	GTATGGCGAG	780
GACATTGAGA	TTTCAGACAC	CGAGAGCTTC	TCCAACGATC	CCTGTACCAG	TGTCAAAAAG	840
CTGAAGGGGA	ATGATGTGCG	GATCATCCTT	GGCCAGTTTG	ACCAGAATAT	GGCAGCAAAA	900
GTGTTCTGTT	GTGCATACGA	GGAGAACATG	TATGGTAGTA	AATATCAGTG	GATCATTCCG	960
GGCTGGTACG	AGCCTTCTTG	GTGGGAGCAG	GTGCACACGG	AAGCCAACTC	ATCCCCTGTC	1020
CTCCGGAAGA	ATCTGCTTGC	TGCCATGGAG	GGCTACATTG	GCGTGGATTT	CGAGCCCCTG	1080
AGCTCCAAGC	AGATCAAGAC	CATCTCAGGA	AAGACTCCAC	AGCAGTATGA	GAGAGAGTAC	1140
AACAACAAGC	GGTCAGGCGT	GGGGCCCAGC	AAGTTCCACG	GGTACGCCTA	CGATGGCATC	1200
TGGGTCATCG	CCAAGACACT	GCAGAGGGCC	ATGGAGACAC	TGCATGCCAG	CAGCCGGCAC	1260
CAGCGGATCC	AGGACTTCAA	CTACACGGAC	CACACGCTGG	GCAGGATCAT	CCTCAATGCC	1320
ATGAACGAGA	CCAACTTCTT	CGGGGTCACG	GGTCAAGTTG	TATTCCGGAA	TGGGGAGAGA	1380
ATGGGGACCA	TTAAATTTAC	TCAATTTCAA	GACAGCAGGG	AGGTGAAGGT	GGGAGAGTAC	1440
AACGCTGTGG	CCGACACACT	GGAGATCATC	AATGACACCA	TCAGGTTCCA	AGGATCCGAA	1500
CCACCAAAAG	ACAAGACCAT	CATCCTGGAG	CAGCTGCGGA	AGATCTCCCT	ACCTCTCTAC	1560
AGCATCCTCT	CTGCCCTCAC	CATCCTCGGG	ATGATCATGG	CCAGTGCTTT	TCTCTTCTTC	1620
AACATCAAGA	ACCGGAATCA	GAAGCTCATA	AAGATGTCGA	GTCCATACAT	GAACAACCTT	1680
ATCATCCTTG	GAGGGATGCT	TTCTATGCT	TCCATATTTT	TCTTTGGCCT	TGATGGATCC	1740
TTTGTCTCTG	AAAAGACCTT	TGAAACACTT	TGCACCGTCA	GGACCTGGAT	TCTCACCGTG	1800
GGCTACACGA	CCGCTTTTGG	GGCCATGTTT	GCAAAGACCT	GGAGAGTCCA	CGCCATCTTC	1860
AAAAATGTGA	AAATGAAGAA	GAAGATCATC	AAGGACCAGA	AACTGCTTGT	GATCGTGGGG	1920
GGCATGCTGC	TGATCGACCT	GTGTATCCTG	ATCTGCTGGC	AGGCTGTGGA	CCCCCTGCGA	1980
AGGACAGTGG	AGAAGTACAG	CATGGAGCCG	GACCCAGCAG	GACGGGATAT	CTCCATCCGC	2040
CCTCTCCTGG	AGCACTGTGA	GAACACCCAT	ATGACCATCT	GGCTTGGCAT	CGTCTATGCC	2100

TACAAGGGAC TTCTCATGTT GTTCGGTTGT TTCTTAGCTT GGGAGACCCG CAACGTCAGC 2160
 ATCCCCGCAC TCAACGACAG CAAGTACATC GGGATGAGTG TCTACAACGT GGGGATCATG 2220
 TGCATCATCG GGGCCGCTGT CTCCTTCCTG ACCCGGGACC AGCCCAATGT GCAGTTCTGC 2280
 ATCGTGGCTC TGGTCATCAT CTTCTGCAGC ACCATCACCC TCTGCCTGGT ATTCGTGCCG 2340
 AAGCTCATCA CCCTGAGAAC AAACCCAGAT GCAGCAACGC AGAACAGGCG ATTCCAGTTC 2400
 ACTCAGAATC AGAAGAAAGA AGATTCTAAA ACGTCCACCT CGGTCACCAG TGTGAACCAA 2460
 GCCAGCACAT CCCGCCTGGA GGGCCTACAG TCAGAAAACC ATCGCCTGCG AATGAAGATC 2520
 ACAGAGCTGG ATAAAGACTT GGAAGAGGTC ACCATGCAGC TGCAGGACAC ACCAGAAAAG 2580
 ACCACCTACA TTAAACAGAA CCACTACCAA GAGCTCAATG ACATCCTCAA CCTGGGAAAC 2640
 TTCACTGAGA GCACAGATGG AGGAAAGGCC ATTTTAAAAA ATCACCTCGA TCAAAATCCC 2700
 CAGCTACAGT GGAACACAAC AGAGCCCTCT CGAACATGCA AAGATCCTAT AGAAGATATA 2760
 AACTCTCCAG AACACATCCA GCGTCGGCTG TCCCTCCAGC TCCCCATCCT CCACCACGCC 2820
 TACCTCCCAT CCATCGGAGG CGTGGACGCC AGCTGTGTCA GCCCTGCGT CAGCCCCACC 2880
 GCCAGCCCCC GCCACAGACA TGTGCCACCC TCCTTCCGAG TCATGGTCTC GGGCCTGTAA 2940
 GGGTGGGAGG CCTGGGCCCC GGGCCTCCCC CGTGACAGAA CCACACTGGG CAGAGGGGTC 3000
 TGCTGCAGAA AACTGTTCGG CTCTGGCTGC GGAGAAGCTG GGCACCATGG CTGGCCTCTC 3060
 AGGACCACTC GGATGGCACT CAGGTGGACA GGACGGGGCA GGGGGAGACT TGGCACCTGA 3120
 CCTCGAGCCT TATTTGTGAA GTCCTTATTT CTTACAAAAG AAGAGGAACG GAAATGGGAC 3180
 GTCTTCCTTA ACATCTGCAA ACAAGGAGGC GCTGGGATAT CAAACTTGCA AAAAAAAAAA 3240
 AAAA 3244

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 898 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Pro Ser Cys Pro Ala Arg Ser Ala Thr Gly Pro Leu Ser Ile Met
 1 5 10 15
 Gly Leu Met Pro Leu Thr Lys Glu Val Ala Lys Gly Ser Ile Gly Arg
 20 25 30

Figure 1: A multi-panel figure showing the effect of 100% O₂ on various parameters. The top panel is a bar graph of 'Relative survival (%)' for 'Control' and '100% O₂' groups. The middle panel is a line graph of 'Survival (%)' over 'Time (h)' for 'Control' and '100% O₂' groups. The bottom panel is a bar graph of 'Relative survival (%)' for 'Control' and '100% O₂' groups. The figure is labeled 'Figure 1' and 'Figure 2'.

Thr Gly Gln Val Val Phe Arg Asn Gly Glu Arg Met Gly Thr Ile Lys
 370 375 380
 Phe Thr Gln Phe Gln Asp Ser Arg Glu Val Lys Val Gly Glu Tyr Asn
 385 390 395 400
 Ala Val Ala Asp Thr Leu Glu Ile Ile Asn Asp Thr Ile Arg Phe Gln
 405 410 415
 Gly Ser Glu Pro Pro Lys Asp Lys Thr Ile Ile Leu Glu Gln Leu Arg
 420 425 430
 Lys Ile Ser Leu Pro Leu Tyr Ser Ile Leu Ser Ala Leu Thr Ile Leu
 435 440 445
 Gly Met Ile Met Ala Ser Ala Phe Leu Phe Phe Asn Ile Lys Asn Arg
 450 455 460
 Asn Gln Lys Leu Ile Lys Met Ser Ser Pro Tyr Met Asn Asn Leu Ile
 465 470 475 480
 Ile Leu Gly Gly Met Leu Ser Tyr Ala Ser Ile Phe Leu Phe Gly Leu
 485 490 495
 Asp Gly Ser Phe Val Ser Glu Lys Thr Phe Glu Thr Leu Cys Thr Val
 500 505 510
 Arg Thr Trp Ile Leu Thr Val Gly Tyr Thr Thr Ala Phe Gly Ala Met
 515 520 525
 Phe Ala Lys Thr Trp Arg Val His Ala Ile Phe Lys Asn Val Lys Met
 530 535 540
 Lys Lys Lys Ile Ile Lys Asp Gln Lys Leu Leu Val Ile Val Gly Gly
 545 550 555 560
 Met Leu Leu Ile Asp Leu Cys Ile Leu Ile Cys Trp Gln Ala Val Asp
 565 570 575
 Pro Leu Arg Arg Thr Val Glu Lys Tyr Ser Met Glu Pro Asp Pro Ala
 580 585 590
 Gly Arg Asp Ile Ser Ile Arg Pro Leu Leu Glu His Cys Glu Asn Thr
 595 600 605
 His Met Thr Ile Trp Leu Gly Ile Val Tyr Ala Tyr Lys Gly Leu Leu
 610 615 620
 Met Leu Phe Gly Cys Phe Leu Ala Trp Glu Thr Arg Asn Val Ser Ile
 625 630 635 640
 Pro Ala Leu Asn Asp Ser Lys Tyr Ile Gly Met Ser Val Tyr Asn Val
 645 650 655
 Gly Ile Met Cys Ile Ile Gly Ala Ala Val Ser Phe Leu Thr Arg Asp
 660 665 670
 Gln Pro Asn Val Gln Phe Cys Ile Val Ala Leu Val Ile Ile Phe Cys
 675 680 685
 Ser Thr Ile Thr Leu Cys Leu Val Phe Val Pro Lys Leu Ile Thr Leu
 690 695 700

Arg Thr Asn Pro Asp Ala Ala Thr Gln Asn Arg Arg Phe Gln Phe Thr
 705 710 715 720
 Gln Asn Gln Lys Lys Glu Asp Ser Lys Thr Ser Thr Ser Val Thr Ser
 725 730 735
 Val Asn Gln Ala Ser Thr Ser Arg Leu Glu Gly Leu Gln Ser Glu Asn
 740 745 750
 His Arg Leu Arg Met Lys Ile Thr Glu Leu Asp Lys Asp Leu Glu Glu
 755 760 765
 Val Thr Met Gln Leu Gln Asp Thr Pro Glu Lys Thr Thr Tyr Ile Lys
 770 775 780
 Gln Asn His Tyr Gln Glu Leu Asn Asp Ile Leu Asn Leu Gly Asn Phe
 785 790 795 800
 Thr Glu Ser Thr Asp Gly Gly Lys Ala Ile Leu Lys Asn His Leu Asp
 805 810 815
 Gln Asn Pro Gln Leu Gln Trp Asn Thr Thr Glu Pro Ser Arg Thr Cys
 820 825 830
 Lys Asp Pro Ile Glu Asp Ile Asn Ser Pro Glu His Ile Gln Arg Arg
 835 840 845
 Leu Ser Leu Gln Leu Pro Ile Leu His His Ala Tyr Leu Pro Ser Ile
 850 855 860
 Gly Gly Val Asp Ala Ser Cys Val Ser Pro Cys Val Ser Pro Thr Ala
 865 870 875 880
 Ser Pro Arg His Arg His Val Pro Pro Ser Phe Arg Val Met Val Ser
 885 890 895
 Gly Leu

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2823 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGCTTCCC CGCCGAGCTC CGGGCAGCCC CGGCCGCCGC CGCCGCCGCC GCCGCCCCGC 60
 CGCCTGCTGC TGCCCCCTGCT GCTGTCGCTG CTGCTGTGGT TGGCGCCCGG GGCCTGGGGC 120
 TGGACGCGGG GCGCCCCCGG GCCGCCGCC AGCAGCCCGC CGCTCTCCAT CATGGGCCTC 180

09011755-121500

ATGCCGCTCA CCAAGGAGGT GGCCAAGGGC AGCATCGGGC GCGGCGTGCT CCCC GCCGTG	240
GAGCTAGCCA TCGAGCAGAT CCGCAACGAG TCACTCCTGC GCCCTACTT CCTGGACCTG	300
CGACTCTATG ACACCGAGTG TGACAATGCA AAGGGACTGA AAGCCTTCTA TGACGCAATA	360
AAGTATGGGC CGAACCATTT GATGGTGT TT GGAGGCGTCT GTCCGTCTGT CACATCTATT	420
ATCGCGGAGT CCCTCCAAGG CTGGAATCTG GTGCAGCTTT CCTTCGCCGC CACCACGCCT	480
GTTCTTGCGG ATAAGAAGAA GTACCCGTAT TTCTTCCGGA CGGTGCCGTC AGACAACGCG	540
GTGAACCCCG CCATCCTGAA GCTCCTGAAG CACTTCCGCT GGCGGCGTGT GGGCACACTC	600
ACGCAGGACG TGCAGCGCTT CTCCGAGGTG AGGAATGACC TGA CTGGGGT TCTGTATGGG	660
GAAGATATTG AGATCTCAGA CACAGAGAGT TTCTCCAATG ATCCCTGCAC CAGCGTCAAA	720
AAGCTCAAGG GGAATGACGT GCGGATCATC CTTGGCCAGT TTGACCAGAA TATGGCAGCA	780
AAAGTCTTCT GTTGTGCCTT CGAGGAGAGC ATGTTTGGCA GCAAGTACCA GTGGATCATC	840
CCGGGATGGT ACGAGCCTGC GTGGTGGGAG CAGGTGCATG TGGAGGCCAA TTCCTCACGC	900
TGCCTGCGCA GAAGCCTCCT GGCTGCCATG GAAGGTTACA TCGGAGTGGA CTTTGAGCCC	960
CTGAGCTCCA AACAAATCAA GACCATCTCA GGGAAGACTC CACAGCAGTA TGAAAGAGAG	1020
TACAACAGCA AACGTT CAGG CGTGGGGCCC AGCAAGTTCC ATGGGTACGC CTACGATGGG	1080
ATCTGGGTCA TCGCCAAGAC CCTACAGAGG GCCATGGAGA CACTGCATGC CAGTAGCAGG	1140
CACCAGCGGA TCCAGGACTT CAACTACACA GACCACACGC TGGGCAAAAT CATCCTCAAT	1200
GCCATGAACG AGACCAACTT CTTCGGGGTC ACGGGTCAAG TTGTGTTCCG GAACGGGGAG	1260
AGAATGGGAA CCATTAAATT TACTCAATTT CAAGACAGCA GAGAGGTGAA GGTGCGCGAA	1320
TACAACGCGG TGGCTGACAC ACTGGAGATC ATCAATGACA CCATAAGGTT CCAGGGGTCC	1380
GAGCCACCCA AGGACAAGAC CATCATTTCTG GAGCAGCTTC GGAAGATCTC GCTTCCACTG	1440
TATAGCATCC TGTCCGCTCT CACCATCCTC GGCATGATCA TGGCCAGCGC CTCCTCTTC	1500
TTCAACATCA AGAACC GGAA CAAAAGCTG ATTAAGATGT CAAGCCCCTA CATGAACAAC	1560
CTCATCATCC TGGGAGGAAT GCTGTCCTAT GCATCCATCT TCCTCTTTGG CCTCGATGGG	1620
TCCTTCGTCT CAGAAAAGAC CTTTGAAACA CTCTGCACGG TCCGGACCTG GATTCTCACC	1680
GTGGGCTACA CAACTGCCTT TGGGGCCATG TTTGCAAAGA CCTGGAGGGT CCATGCCATC	1740
TTCAAAAATG TGAAGATGAA GAAGAAGATC ATCAAAGACC AGAAGCTGCT TGTGATTGTG	1800
GGGGGCATGC TGCTCATCGA CCTGTGCATC CTGATCTGTT GGCAGGCTGT GGACCCCTG	1860
CGGAGGACAG TAGAGAGGTA CAGCATGGAG CCGGACCCAG CAGGCCGGGA CATCTCCATC	1920
CGCCCATTCG TGGAACACTG CGAAAACACC CACATGACCA TCTGGCTTGG CATTGTCTAC	1980
GCCTACAAGG GGCTCCTCAT GCTATTCCGT TGTCTCTTGG CATGGGAAAC CCGCAATGTG	2040
AGCATCCCTG CCCTCAACGA CAGCAAGTAC ATCGGCATGA GTGTGTACAA TGTGGGGATC	2100

ATGTGCATCA TCGGGGCTGC TGTCTCCTTC CTGACGCGTG ACCAGCCCAA CGTGCAGTTC 2160
 TGCATCGTGG CCCTGGTCAT CATCTTCTGC AGCACCATCA CTCTCTGCCT GGTGTTTGTG 2220
 CCAAAGCTCA TTA CTCTGAG GACAAACCCT GACGCAGCCA CTCAGAACAG GCGGTTCAG 2280
 TTCACACAGA ACCAGAAGAA AGAAGATTCG AAGACCTCCA CTTCAGTCAC CAGCGTGAAC 2340
 CAGGCGAGCA CGTCACGCCT GGAGGGACTG CAGTCAGAAA ACCACCGCCT TCGAATGAAG 2400
 ATCACAGAGC TGGACAAAGA CTTGGAAGAA GTCACCATGC AGCTACAAGA CACACCAGAG 2460
 AAGACCACAT ACATCAAACA GAATCACTAC CAAGAGCTCA ACGACATCCT CAGCTTGGGC 2520
 AACTTCACAG AGAGCACAGA TGGAGGAAAG GCCATTCTAA AAAATCACCT CGATCAAAAC 2580
 CCCCAGCTCC AGTGAACAC GACAGAGCCC TCAAGAACAT GCAAAGACCC CATAGAAGAC 2640
 ATCAACTCCC CGGAGCACAT CCAGCGCCGG CTGTCGCTCC AGCTCCCCAT CTTTACCAC 2700
 GCCTACCTCC CATCCATCGG AGGCGTGGAT GCCAGCTGCG TCAGCCCCTG TGTGAGCCCT 2760
 ACCGCCAGCC CTCGCCACAG ACACGTACCA CCCTCCTTCC GAGTCATGGT CTCGGGCCTG 2820
 TAG 2823

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 940 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Ser Pro Pro Ser Ser Gly Gln Pro Arg Pro Pro Pro Pro Pro
 1 5 10 15
 Pro Pro Pro Ala Arg Leu Leu Leu Pro Leu Leu Leu Ser Leu Leu Leu
 20 25 30
 Trp Leu Ala Pro Gly Ala Trp Gly Trp Thr Arg Gly Ala Pro Arg Pro
 35 40 45
 Pro Pro Ser Ser Pro Pro Leu Ser Ile Met Gly Leu Met Pro Leu Thr
 50 55 60
 Lys Glu Val Ala Lys Gly Ser Ile Gly Arg Gly Val Leu Pro Ala Val
 65 70 75 80
 Glu Leu Ala Ile Glu Gln Ile Arg Asn Glu Ser Leu Leu Arg Pro Tyr
 85 90 95
 Phe Leu Asp Leu Arg Leu Tyr Asp Thr Glu Cys Asp Asn Ala Lys Gly

145

100					105					110					
Leu	Lys	Ala	Phe	Tyr	Asp	Ala	Ile	Lys	Tyr	Gly	Pro	Asn	His	Leu	Met
		115					120					125			
Val	Phe	Gly	Gly	Val	Cys	Pro	Ser	Val	Thr	Ser	Ile	Ile	Ala	Glu	Ser
	130					135					140				
Leu	Gln	Gly	Trp	Asn	Leu	Val	Gln	Leu	Ser	Phe	Ala	Ala	Thr	Thr	Pro
145					150					155					160
Val	Leu	Ala	Asp	Lys	Lys	Lys	Tyr	Pro	Tyr	Phe	Phe	Arg	Thr	Val	Pro
				165					170					175	
Ser	Asp	Asn	Ala	Val	Asn	Pro	Ala	Ile	Leu	Lys	Leu	Leu	Lys	His	Phe
			180					185					190		
Arg	Trp	Arg	Arg	Val	Gly	Thr	Leu	Thr	Gln	Asp	Val	Gln	Arg	Phe	Ser
		195					200					205			
Glu	Val	Arg	Asn	Asp	Leu	Thr	Gly	Val	Leu	Tyr	Gly	Glu	Asp	Ile	Glu
	210					215					220				
Ile	Ser	Asp	Thr	Glu	Ser	Phe	Ser	Asn	Asp	Pro	Cys	Thr	Ser	Val	Lys
225					230					235					240
Lys	Leu	Lys	Gly	Asn	Asp	Val	Arg	Ile	Ile	Leu	Gly	Gln	Phe	Asp	Gln
				245					250					255	
Asn	Met	Ala	Ala	Lys	Val	Phe	Cys	Cys	Ala	Phe	Glu	Glu	Ser	Met	Phe
			260					265					270		
Gly	Ser	Lys	Tyr	Gln	Trp	Ile	Ile	Pro	Gly	Trp	Tyr	Glu	Pro	Ala	Trp
		275					280					285			
Trp	Glu	Gln	Val	His	Val	Glu	Ala	Asn	Ser	Ser	Arg	Cys	Leu	Arg	Arg
	290					295					300				
Ser	Leu	Leu	Ala	Ala	Met	Glu	Gly	Tyr	Ile	Gly	Val	Asp	Phe	Glu	Pro
305					310					315					320
Leu	Ser	Ser	Lys	Gln	Ile	Lys	Thr	Ile	Ser	Gly	Lys	Thr	Pro	Gln	Gln
				325					330					335	
Tyr	Glu	Arg	Glu	Tyr	Asn	Ser	Lys	Arg	Ser	Gly	Val	Gly	Pro	Ser	Lys
			340					345					350		
Phe	His	Gly	Tyr	Ala	Tyr	Asp	Gly	Ile	Trp	Val	Ile	Ala	Lys	Thr	Leu
		355					360					365			
Gln	Arg	Ala	Met	Glu	Thr	Leu	His	Ala	Ser	Ser	Arg	His	Gln	Arg	Ile
	370					375					380				
Gln	Asp	Phe	Asn	Tyr	Thr	Asp	His	Thr	Leu	Gly	Lys	Ile	Ile	Leu	Asn
385					390					395					400
Ala	Met	Asn	Glu	Thr	Asn	Phe	Phe	Gly	Val	Thr	Gly	Gln	Val	Val	Phe
				405					410					415	
Arg	Asn	Gly	Glu	Arg	Met	Gly	Thr	Ile	Lys	Phe	Thr	Gln	Phe	Gln	Asp
			420					425					430		
Ser	Arg	Glu	Val	Lys	Val	Gly	Glu	Tyr	Asn	Ala	Val	Ala	Asp	Thr	Leu

0924755 "121598

435					440					445					
Glu	Ile	Ile	Asn	Asp	Thr	Ile	Arg	Phe	Gln	Gly	Ser	Glu	Pro	Pro	Lys
450						455					460				
Asp	Lys	Thr	Ile	Ile	Leu	Glu	Gln	Leu	Arg	Lys	Ile	Ser	Leu	Pro	Leu
465					470					475					480
Tyr	Ser	Ile	Leu	Ser	Ala	Leu	Thr	Ile	Leu	Gly	Met	Ile	Met	Ala	Ser
				485					490					495	
Ala	Phe	Leu	Phe	Phe	Asn	Ile	Lys	Asn	Arg	Asn	Gln	Lys	Leu	Ile	Lys
			500					505					510		
Met	Ser	Ser	Pro	Tyr	Met	Asn	Asn	Leu	Ile	Ile	Leu	Gly	Gly	Met	Leu
		515				520						525			
Ser	Tyr	Ala	Ser	Ile	Phe	Leu	Phe	Gly	Leu	Asp	Gly	Ser	Phe	Val	Ser
	530					535					540				
Glu	Lys	Thr	Phe	Glu	Thr	Leu	Cys	Thr	Val	Arg	Thr	Trp	Ile	Leu	Thr
545					550					555					560
Val	Gly	Tyr	Thr	Thr	Ala	Phe	Gly	Ala	Met	Phe	Ala	Lys	Thr	Trp	Arg
				565				570						575	
Val	His	Ala	Ile	Phe	Lys	Asn	Val	Lys	Met	Lys	Lys	Lys	Ile	Ile	Lys
			580					585					590		
Asp	Gln	Lys	Leu	Leu	Val	Ile	Val	Gly	Gly	Met	Leu	Leu	Ile	Asp	Leu
		595				600						605			
Cys	Ile	Leu	Ile	Cys	Trp	Gln	Ala	Val	Asp	Pro	Leu	Arg	Arg	Thr	Val
	610					615					620				
Glu	Arg	Tyr	Ser	Met	Glu	Pro	Asp	Pro	Ala	Gly	Arg	Asp	Ile	Ser	Ile
625					630					635					640
Arg	Pro	Leu	Leu	Glu	His	Cys	Glu	Asn	Thr	His	Met	Thr	Ile	Trp	Leu
				645				650						655	
Gly	Ile	Val	Tyr	Ala	Tyr	Lys	Gly	Leu	Leu	Met	Leu	Phe	Gly	Cys	Phe
			660					665					670		
Leu	Ala	Trp	Glu	Thr	Arg	Asn	Val	Ser	Ile	Pro	Ala	Leu	Asn	Asp	Ser
		675				680						685			
Lys	Tyr	Ile	Gly	Met	Ser	Val	Tyr	Asn	Val	Gly	Ile	Met	Cys	Ile	Ile
	690					695					700				
Gly	Ala	Ala	Val	Ser	Phe	Leu	Thr	Arg	Asp	Gln	Pro	Asn	Val	Gln	Phe
705					710					715					720
Cys	Ile	Val	Ala	Leu	Val	Ile	Ile	Phe	Cys	Ser	Thr	Ile	Thr	Leu	Cys
				725				730						735	
Leu	Val	Phe	Val	Pro	Lys	Leu	Ile	Thr	Leu	Arg	Thr	Asn	Pro	Asp	Ala
			740					745					750		
Ala	Thr	Gln	Asn	Arg	Arg	Phe	Gln	Phe	Thr	Gln	Asn	Gln	Lys	Lys	Glu
		755				760						765			
Asp	Ser	Lys	Thr	Ser	Thr	Ser	Val	Thr	Ser	Val	Asn	Gln	Ala	Ser	Thr

(iv) ANTI-SENSE: NO

CAATGTGCAG TTCTGCATCG TGGCTCTGGT CATCATCTTC TGCAG

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTTCTAGGCC TGTACGGAAG TGTT

24

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTTGTGGTTT GTCCAAACTC ATCAAT

26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGATGAGTG TCTACAACGT GGGG

24

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGCGTTGCTG CATCTGGGTT TGTTC

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCTCCCTAC CTCTCTACAG CATCCT

26

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAGGTCCTGA CGGTGCAAAG TGTTTC

26

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:

363177-363178

```
(ii) MOLECULE TYPE: other nucleic acid
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: NO
```

TGACGCAAGA CGTTCAGAGG TTCTCT

(2) INFORMATION FOR SEQ ID NO:14:

(ii) MOLECULE TYPE: other nucleic acid

(iv) ANTI-SENSE: NO

TGTAGCCTTC CATGGCAGCA AGCAGA

(2) INFORMATION FOR SEQ ID NO:15:

(ii) MOLECULE TYPE: other nucleic acid

(iv) ANTI-SENSE: NO

AGAGAACCTC TGAACGTCTT GCGTCA

(2) INFORMATION FOR SEQ ID NO:16:

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCTCTGTTG TGTTCCACTG TAGCTG

26

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCATGCCGCT CACCAAGGAG GTGGCC

26

2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGCCACCTCC TTGGTGAGCG GCATGA

26

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

0921755-421598

TGAGTGAGCA GAGTCCAGAG CCGT

24

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATGGATGGGA GGTAGGCGTG GTGGAG

26

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CTCTCTGCCC TCACCATCCT CGGGAT

26

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GACTCCGGCT CGAATACCAG GCAGAG

26

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:

004475-121598

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCATGTTTGC AAAGACCTGG AGGGTCC

27

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGTCACGCGT CAGGAAAGAG ACAGCAG

27

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AAGCTTCTAG AGATCCCTCG ACCTC

25

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iv) ANTI-SENSE: NO

AGGCGCAGAA CTGGTAGGTA TGGAA

25

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTTCTAGGCC TGTACGGAAG TGTTA

25

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTTGTGGTTT GTCCAAAC TC ATCAATG

27

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CTGCTGTCTC TTCCTGACG CGTGACC

27

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CCAAGCTTCT AATACGACTC ACTATAGGGG AGACCATGGG CCCGGGGGGA CCCTGTACC

59

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CACTTGTAAG GCAAATGTAC TCGACTCC

28

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CGCGGATCCA TTATGTCTGC ACTCCGAAGG AAATTTG

37

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGCGAATTCT TATGTGAAGC GATCAGAGTT CATTTTTC

38

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

CGGGGATCCG CTATGGCTGG TGATTCTAGG AATG

34

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCGGAATTCC CCTCACACCG AGCCCCTGG

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:

091156-121598

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCAATAAAGT ATGGGCTGAA CCATTTGATG GTGTTTGGAG GCGT

44

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 44 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ACGCCTCCAA ACACCATCAA ATGGTTCAGC CCATACTTTA TTGC

44

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTGAGCCCC TGAGCTCCAA ACAAATCAAG ACCATCTCAG

40

(2) INFORMATION FOR SEQ ID NO:39:

09011755-11500
065737-527260

```
(ii) MOLECULE TYPE: DNA (genomic).
(iii) HYPOTHETICAL: NO
(iv) ANTI-SENSE: YES
```

CTGAGATGGT CTTGATTTGT TTGGAGCTCA GGGGCTCAAA

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

AAGGCCATCA ACTTCCTGCC TGTGGACTAT GAGATCGAAT ATG

43

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 43 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

CATATTCGAT CTCATAGTCC ACAGGCAGGA AGTTGATGGC CTT

43

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TGGCCGCTGC CTCTTCTGCT GGTGATGGCG GCTGGGGT

38

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACCCAGCCG CCATCACCAG CAGAAGAGGC AGCGGCCA

38

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 45 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

365TAT"554T260

CCTTGGCTTT GGCCTTGAAC AAGACGTCTG GAGGAGGTGG TCGTT

45

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

AACGACCACC TCCTCCAGAC GTCTTGTTCA AGGCCAAAGC CAAGG

45

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2826 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATGGCTTCCC CGCGGAGCTC CGGGCAGCCC GGGCCGCCGC CGCCGCCGCC ACCGCCGCCC	60
GCGCGCCTGC TACTGCTACT GCTGCTGCCG CTGCTGCTGC CTCTGGCGCC CGGGGCCTGG	120
GGCTGGGCGC GGGGCGCCCC CCGGCCGCCG CCCAGCAGCC CGCCGCTCTC CATCATGGGC	180
CTCATGCCGC TCACCAAGGA GGTGGCCAAG GGCAGCATCG GGCGCGGTGT GCTCCCCGCC	240
GTGGAAGTGG CCATCGAGCA GATCCGCAAC GAGTCACTCC TGCGCCCCTA CTTCTCTGAC	300
CTGCGGCTCT ATGACACGGA GTGCGACAAC GCAAAGGGT TGAAAGCCTT CTACGATGCG	360
ATAAAATACG GGCCGAACCA CTTGATGGTG TTTGGAGGCG TCTGTCCATC CGTCACATCC	420
ATCATTGCAG AGTCCCTCCA AGGCTGGAAT CTGGTGCAGC TTTCTTTTGC TGCAACCACG	480
CCTGTTCTAG CCGATAAGAA AAAATACCCT TATTTCTTTC GGACCGTCCC ATCAGACAAT	540
GCGGTGAATC CAGCCATTCT GAAAGTGCTC AAGCACTACC AGTGGAAGCG CGTGGGCAGC	600

CTGACGCAAG	ACGTTTCAGAG	GTTCTCTGAG	GTGCGGAATG	ACCTGACTGG	AGTTCTGTAT	660
GGCGAGGACA	TTGAGATTTC	AGACACCGAG	AGCTTCTCCA	ACGATCCCTG	TACCAGTGTC	720
AAAAAGCTGA	AGGGGAATGA	TGTGCGGATC	ATCCTTGGCC	AGTTTGACCA	GAATATGGCA	780
GCAAAAGTGT	TCTGTTGTGC	ATACGAGGAG	AACATGTATG	GTAGTAAATA	TCAGTGGATC	840
ATTCCGGGCT	GGTACGAGCC	TTCTTGGTGG	GAGCAGGTGC	ACACGGAAGC	CAACTCATCC	900
CGCTGCCTCC	GGAAGAATCT	GCTTGCTGCC	ATGGAGGGCT	ACATTGGCGT	GGATTTCGAG	960
CCCCTGAGCT	CCAAGCAGAT	CAAGACCATC	TCAGGAAAGA	CTCCACAGCA	GTATGAGAGA	1020
GAGTACAACA	ACAAGCGGTC	AGGCGTGGGG	CCCAGCAAGT	TCCACGGGTA	CGCCTACGAT	1080
GGCATCTGGG	TCATCGCCAA	GACACTGCAG	AGGGCCATGG	AGACACTGCA	TGCCAGCAGC	1140
CGGCACCAGC	GGATCCAGGA	CTTCAACTAC	ACGGACCACA	CGCTGGGCAG	GATCATCCTC	1200
AATGCCATGA	ACGAGACCAA	CTTCTTCGGG	GTCACGGGTC	AAGTTGTATT	CCGGAATGGG	1260
GAGAGAATGG	GGACCATTAA	ATTTACTCAA	TTTCAAGACA	GCAGGGAGGT	GAAGGTGGGA	1320
GAGTACAACG	CTGTGGCCGA	CACACTGGAG	ATCATCAATG	ACACCATCAG	GTTCCAAGGA	1380
TCCGAACCAC	CAAAAGACAA	GACCATCATC	CTGGAGCAGC	TGCGGAAGAT	CTCCCTACCT	1440
CTCTACAGCA	TCCTCTCTGC	CCTCACCATC	CTCGGGATGA	TCATGGCCAG	TGCTTTTCTC	1500
TTCTTCAACA	TCAAGAACCG	GAATCAGAAG	CTCATAAAGA	TGTCGAGTCC	ATACATGAAC	1560
AACCTTATCA	TCCTTGGAGG	GATGCTTTCC	TATGCTTCCA	TATTTCTCTT	TGGCCTTGAT	1620
GGATCCTTTG	TCTCTGAAAA	GACCTTTGAA	ACACTTTGCA	CCGTCAGGAC	CTGGATTCTC	1680
ACCGTGGGCT	ACACGACCGC	TTTTGGGGCC	ATGTTTGCAA	AGACCTGGAG	AGTCCACGCC	1740
ATCTTCAAAA	ATGTGAAAAT	GAAGAAGAAG	ATCATCAAGG	ACCAGAAACT	GCTTGTGATC	1800
GTGGGGGGCA	TGCTGCTGAT	CGACCTGTGT	ATCCTGATCT	GCTGGCAGGC	TGTGGACCCC	1860
CTGCGAAGGA	CAGTGGAGAA	GTACAGCATG	GAGCCGGACC	CAGCAGGACG	GGATATCTCC	1920
ATCCGCCCTC	TCCTGGAGCA	CTGTGAGAAC	ACCCATATGA	CCATCTGGCT	TGGCATCGTC	1980
TATGCCTACA	AGGGACTTCT	CATGTTGTTC	GGTTGTTTCT	TAGCTTGGGA	GACCCGCAAC	2040
GTCAGCATCC	CCGCACTCAA	CGACAGCAAG	TACATCGGGA	TGAGTGTCTA	CAACGTGGGG	2100
ATCATGTGCA	TCATCGGGGC	CGCTGTCTCC	TTCTTGACCC	GGGACCAGCC	CAATGTGCAG	2160
TTCTGCATCG	TGGCTCTGGT	CATCATCTTC	TGCAGCACCA	TCACCCTCTG	CCTGGTATTC	2220
GTGCCGAAGC	TCATCACCCCT	GAGAACAAAC	CCAGATGCAG	CAACGCAGAA	CAGGCGATTG	2280
CAGTTCACTC	AGAATCAGAA	GAAAGAAGAT	TCTAAAACGT	CCACCTCGGT	CACCAAGTGTG	2340
AACCAAGCCA	GCACATCCCG	CCTGGAGGGC	CTACAGTCAG	AAAACCATCG	CCTGCGAATG	2400
AAGATCACAG	AGCTGGATAA	AGACTTGGA	GAGGTCACCA	TGCAGCTGCA	GGACACACCA	2460
GAAAAGACCA	CCTACATTAA	ACAGAACCAC	TACCAAGAGC	TCAATGACAT	CCTCAACCTG	2520

GGAAACTTCA CTGAGAGCAC AGATGGAGGA AAGGCCATTT TAAAAAATCA CCTCGATCAA 2580
 AATCCCCAGC TACAGTGGAA CACAACAGAG CCCTCTCGAA CATGCAAAGA TCCTATAGAA 2640
 GATATAAACT CTCCAGAACA CATCCAGCGT CGGCTGTCCC TCCAGCTCCC CATCCTCCAC 2700
 CACGCCTACC TCCCATCCAT CGGAGGCGTG GACGCCAGCT GTGTCAGCCC CTGCGTCAGC 2760
 CCCACCGCCA GCCCCCGCCA CAGACATGTG CCACCCTCCT TCCGAGTCAT GGTCTCGGGC 2820
 CTGTAA 2826

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 941 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: not relevant

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met	Ala	Ser	Pro	Arg	Ser	Ser	Gly	Gln	Pro	Gly	Pro	Pro	Pro	Pro	Pro	Pro	1	5	10	15
Pro	Pro	Pro	Pro	Ala	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	20	25	30	
Leu	Pro	Leu	Ala	Pro	Gly	Ala	Trp	Gly	Trp	Ala	Arg	Gly	Ala	Pro	Arg	Arg	35	40	45	
Pro	Pro	Pro	Ser	Ser	Pro	Pro	Leu	Ser	Ile	Met	Gly	Leu	Met	Pro	Leu	Leu	50	55	60	
Thr	Lys	Glu	Val	Ala	Lys	Gly	Ser	Ile	Gly	Arg	Gly	Val	Leu	Pro	Ala	Ala	65	70	75	80
Val	Glu	Leu	Ala	Ile	Glu	Gln	Ile	Arg	Asn	Glu	Ser	Leu	Leu	Arg	Pro	Pro	85	90	95	
Tyr	Phe	Leu	Asp	Leu	Arg	Leu	Tyr	Asp	Thr	Glu	Cys	Asp	Asn	Ala	Lys	Lys	100	105	110	
Gly	Leu	Lys	Ala	Phe	Tyr	Asp	Ala	Ile	Lys	Tyr	Gly	Pro	Asn	His	Leu	Leu	115	120	125	
Met	Val	Phe	Gly	Gly	Val	Cys	Pro	Ser	Val	Thr	Ser	Ile	Ile	Ala	Glu	Glu	130	135	140	
Ser	Leu	Gln	Gly	Trp	Asn	Leu	Val	Gln	Leu	Ser	Phe	Ala	Ala	Thr	Thr	Thr	145	150	155	160
Pro	Val	Leu	Ala	Asp	Lys	Lys	Lys	Tyr	Pro	Tyr	Phe	Phe	Arg	Thr	Val	Val	165	170	175	
Pro	Ser	Asp	Asn	Ala	Val	Asn	Pro	Ala	Ile	Leu	Lys	Leu	Leu	Lys	His	His				

515					520					525					
Leu	Ser	Tyr	Ala	Ser	Ile	Phe	Leu	Phe	Gly	Leu	Asp	Gly	Ser	Phe	Val
	530					535					540				
Ser	Glu	Lys	Thr	Phe	Glu	Thr	Leu	Cys	Thr	Val	Arg	Thr	Trp	Ile	Leu
545					550					555					560
Thr	Val	Gly	Tyr	Thr	Thr	Ala	Phe	Gly	Ala	Met	Phe	Ala	Lys	Thr	Trp
				565					570					575	
Arg	Val	His	Ala	Ile	Phe	Lys	Asn	Val	Lys	Met	Lys	Lys	Lys	Ile	Ile
			580					585					590		
Lys	Asp	Gln	Lys	Leu	Leu	Val	Ile	Val	Gly	Gly	Met	Leu	Leu	Ile	Asp
		595					600					605			
Leu	Cys	Ile	Leu	Ile	Cys	Trp	Gln	Ala	Val	Asp	Pro	Leu	Arg	Arg	Thr
	610					615					620				
Val	Glu	Lys	Tyr	Ser	Met	Glu	Pro	Asp	Pro	Ala	Gly	Arg	Asp	Ile	Ser
625					630					635					640
Ile	Arg	Pro	Leu	Leu	Glu	His	Cys	Glu	Asn	Thr	His	Met	Thr	Ile	Trp
				645					650					655	
Leu	Gly	Ile	Val	Tyr	Ala	Tyr	Lys	Gly	Leu	Leu	Met	Leu	Phe	Gly	Cys
			660					665					670		
Phe	Leu	Ala	Trp	Glu	Thr	Arg	Asn	Val	Ser	Ile	Pro	Ala	Leu	Asn	Asp
		675					680					685			
Ser	Lys	Tyr	Ile	Gly	Met	Ser	Val	Tyr	Asn	Val	Gly	Ile	Met	Cys	Ile
	690					695					700				
Ile	Gly	Ala	Ala	Val	Ser	Phe	Leu	Thr	Arg	Asp	Gln	Pro	Asn	Val	Gln
705					710					715					720
Phe	Cys	Ile	Val	Ala	Leu	Val	Ile	Ile	Phe	Cys	Ser	Thr	Ile	Thr	Leu
			725						730					735	
Cys	Leu	Val	Phe	Val	Pro	Lys	Leu	Ile	Thr	Leu	Arg	Thr	Asn	Pro	Asp
			740					745					750		
Ala	Ala	Thr	Gln	Asn	Arg	Arg	Phe	Gln	Phe	Thr	Gln	Asn	Gln	Lys	Lys
		755					760					765			
Glu	Asp	Ser	Lys	Thr	Ser	Thr	Ser	Val	Thr	Ser	Val	Asn	Gln	Ala	Ser
	770					775					780				
Thr	Ser	Arg	Leu	Glu	Gly	Leu	Gln	Ser	Glu	Asn	His	Arg	Leu	Arg	Met
785					790					795					800
Lys	Ile	Thr	Glu	Leu	Asp	Lys	Asp	Leu	Glu	Glu	Val	Thr	Met	Gln	Leu
				805					810					815	
Gln	Asp	Thr	Pro	Glu	Lys	Thr	Thr	Tyr	Ile	Lys	Gln	Asn	His	Tyr	Gln
			820					825					830		
Glu	Leu	Asn	Asp	Ile	Leu	Asn	Leu	Gly	Asn	Phe	Thr	Glu	Ser	Thr	Asp
		835					840					845			
Gly	Gly	Lys	Ala	Ile	Leu	Lys	Asn	His	Leu	Asp	Gln	Asn	Pro	Gln	Leu

850		855		860
Gln Trp Asn Thr Thr Glu Pro Ser Arg Thr Cys Lys Asp Pro Ile Glu				
865		870	875	880
Asp Ile Asn Ser Pro Glu His Ile Gln Arg Arg Leu Ser Leu Gln Leu				
	885		890	895
Pro Ile Leu His His Ala Tyr Leu Pro Ser Ile Gly Gly Val Asp Ala				
	900		905	910
Ser Cys Val Ser Pro Cys Val Ser Pro Thr Ala Ser Pro Arg His Arg				
	915		920	925
His Val Pro Pro Ser Phe Arg Val Met Val Ser Gly Leu				
	930		935	940

0901755 24593



09/211,755

Examiner Please Note:

This sequence listing follows the Old Rule Format but has a filing date on/after July 1, 1998.

Please determine the effective filing date of the case.

- If it is before July 1, 1998 - Applicants were correct in following the Old Rule Format -
→→ Nothing further needs to be done.
- If it is after July 1, 1998 - Applicants should follow the New Rule Format-
→→ Please request them to submit a new Sequence Listing (both in electronic and paper format) following the New Rule Format.